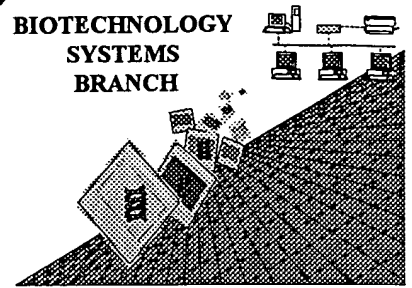


## Exhibit B

FILE COPY

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



*Draper*  
**RAW SEQUENCE LISTING**  
**ERROR REPORT**

FILE COPY

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 08/484,312  
Art Unit / Team No. : 1646  
Date Processed by STIC: 3/22/99

**THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.**

**PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:**

**1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,**

**2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY**

**THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.**

**IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:**

**ARTI SHAH 703-308-4212**

PAGE: 1

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/484,312

DATE: 03/22/1999  
TIME: 13:46:59

INPUT SET: S31121.raw

This Raw Listing contains the General  
Information Section and those Sequences  
containing ERRORS.

## SEQUENCE LISTING

Does Not Comply  
Corrected Diskette Needed

1  
2  
3 (1) General Information:  
4  
5 (i) APPLICANT: Hauptman, et al.  
6  
7 (ii) TITLE OF INVENTION: TNF RECEPTORS, TNF BINDING BINDING PROTEINS, AND DNAs CODIN  
8  
9 (iii) NUMBER OF SEQUENCES: 64 92 (p. 19)  
10  
11 (iv) CORRESPONDENCE ADDRESS:  
12 (A) ADDRESSEE: John J. McDonnell  
13 (B) STREET: 300 S. Wacker Drive  
14 (C) CITY: Chicago  
15 (D) STATE: IL  
16 (E) COUNTRY: USA  
17 (F) ZIP: 60606  
18  
19 (v) COMPUTER READABLE FORM:  
20 (A) MEDIUM TYPE: Floppy disk  
21 (B) COMPUTER: IBM PC compatible  
22 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
23 (D) SOFTWARE: ASCII  
24  
25 (vi) CURRENT APPLICATION DATA:  
26 (A) APPLICATION NUMBER: 08/484,312  
27 (B) FILING DATE: June 7, 1995  
28 (C) CLASSIFICATION:  
29  
30 (viii) ATTORNEY/AGENT INFORMATION:  
31 (A) NAME: John J. McDonnell  
32 (B) REGISTRATION NUMBER: 26,949  
33 (C) REFERENCE/DOCKET NUMBER: 98,385-A  
34  
35 (ix) TELECOMMUNICATION INFORMATION:  
36 (A) TELEPHONE: 312-913-0001  
37 (B) TELEFAX: 312-913-9808  
38

-->

*?*

*selected 3 on Eva summary sheet*

*Suggestion: Consult sequence Rule for label format*

## ERRORED SEQUENCES FOLLOW:

39 (2) INFORMATION FOR SEQ ID NO:1:

# RAW SEQUENCE LISTING

## PATENT APPLICATION US/08/484,312

 DATE: 03/22/1999  
 TIME: 13:46:59

INPUT SET: S31121.rgw

*insert a land return  
 after each cumulative base  
 total - all text must  
 be visible*

40  
 --> 41 (i) SEQUENCE CHARACTERISTICS:  
 42 (A) LENGTH:1365 bases  
 43 (B) TYPE:nucleic acid  
 44 (C) STRANDEDNESS:single  
 45 (D) TOPOLOGY:linear  
 46  
 47 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
 48  
 49 ATGGGCCTCT CCACCGTGCC TGACCTGCTG CTGCCACTGG TGCTCCTGGA 50 GCTGTTGGTG GGAATATACC  
 50

51 (2) INFORMATION FOR SEQ ID NO:2:  
 52  
 --> 53 (i) SEQUENCE CHARACTERISTICS:  
 54 (A) LENGTH:483 bases  
 55 (B) TYPE:nucleic acid  
 56 (C) STRANDEDNESS:single  
 57 (D) TOPOLOGY:linear  
 58  
 59 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:  
 60  
 61 GATAGTGTGT GTCCCAAGG AAAATATATC CACCCTCAAA ATAATTGAT 50 TTGCTGTACC AAGTGCCACA A  
 62

63 (2) INFORMATION FOR SEQ ID NO:3:  
 64  
 --> 65 (i) SEQUENCE CHARACTERISTICS:  
 --> 66 (A) LENGTH:455 amino acids  
 --> 67 (B) TYPE:polypeptide  
 --> 68 (D) TOPOLOGY:insert mandatory leading response for all  
 --> 69 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:  
 70  
 71 Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu  
 72 5 10 15  
 73 Leu Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu  
 74 20 25 30  
 75 Val Pro His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro  
 76 35 40 45  
 77 Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr  
 78 50 55 60  
 79 Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro  
 80 65 70 75  
 81 Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr  
 82 80 85 90  
 83 Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys  
 84 95 100 105  
 85 Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp  
 86 110 115 120  
 87 Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr  
 88 125 130 135  
 89 Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu  
 90 140 145 150

*These are  
 global  
 errors*

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/484,312

DATE: 03/22/1999  
TIME: 13:46:59

INPUT SET: S31121.raw

91	Asn Gly Thr Val	His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val	
92		155	160
93	Cys Thr Cys His	Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val	
94		170	175
95	Ser Cys Ser Asn Cys	Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys	
96		185	190
97	Leu Pro Gln Ile	Glu Asn Val Lys Gly Thr Glu Asp Ser Gly Thr	
98		200	205
99	Thr Val Leu Leu	Pro Leu Val Ile Phe Phe Gly Leu Cys Leu Leu	
100		215	220
101	Ser Leu Leu Phe	Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys	
102		230	235
103	Ser Lys Leu Tyr	Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys	
104		245	250
105	Glu Gly Glu Leu	Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn	
106		260	265
107	Pro Ser Phe Ser	Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe	
108		275	280
109	Ser Pro Val Pro	Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr	
110		290	295
111	Pro Gly Asp Cys	Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala	
112		305	310
113	Pro Pro Tyr Gln	Gly Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala	
114		320	325
115	Ser Asp Pro Ile	Pro Asn Pro Leu Gln Lys Trp Glu Asp Ser Ala	
116		335	340
117	His Lys Pro Gln	Ser Leu Asp Thr Asp Asp Pro Ala Thr Leu Tyr	
118		350	355
119	Ala Val Val Glu	Asn Val Pro Pro Leu Arg Trp Lys Glu Phe Val	
120		365	370
121	Arg Arg Leu Gly	Leu Ser Asp His Glu Ile Asp Arg Leu Glu Leu	
122		380	385
123	Gln Asn Gly Arg	Cys Leu Arg Glu Ala Gln Tyr Ser Met Leu Ala	
124		395	400
125	Thr Trp Arg Arg	Arg Thr Pro Arg Arg Glu Ala Thr Leu Glu Leu	
126		410	415
127	Leu Gly Arg Val	Leu Arg Asp Met Asp Leu Leu Gly Cys Leu Glu	
128		425	430
129	Asp Ile Glu Glu	Ala Leu Cys Gly Pro Ala Ala Leu Pro Pro Ala	
130		440	445
131	Pro Ser Leu Leu	Arg	450
132		455	
133			

134 (2) INFORMATION FOR SEQ ID NO:4:

135

136 (i) SEQUENCE CHARACTERISTICS:

--> 137 (A) LENGTH:161 amino acids

--> 138 (B) TYPE:polypeptide

139

--> 140 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

141

142 Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn

*same now*

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/484,312

DATE: 03/22/1999  
TIME: 13:47:00

INPUT SET: S31121.raw

143		5		10		15
144	Ser Ile Cys Cys Thr	Lys Cys His Lys	Gly Thr Tyr Leu Tyr	Asn		
145		20		25		30
146	Asp Cys Pro Gly Pro	Gly Gln Asp Thr	Asp Cys Arg Glu Cys	Glu		
147		35		40		45
148	Ser Gly Ser Phe Thr	Ala Ser Glu Asn His	Leu Arg His Cys	Leu		
149		50		55		60
150	Ser Cys Ser Lys Cys	Arg Lys Glu Met	Gly Gln Val Glu Ile	Ser		
151		65		70		75
152	Ser Cys Thr Val Asp	Arg Asp Thr Val	Cys Gly Cys Arg Lys	Asn		
153		80		85		90
154	Gln Tyr Arg His Tyr	Trp Ser Glu Asn	Leu Phe Gln Cys	Phe Asn		
155		95		100		105
156	Cys Ser Leu Cys Leu	Asn Gly Thr Val	His Leu Ser Cys	Gln Glu		
157		110		115		120
158	Lys Gln Asn Thr Val	Cys Thr Cys His	Ala Gly Phe Phe	Leu Arg		
159		125		130		135
160	Glu Asn Glu Cys Val	Ser Cys Ser Asn	Cys Lys Lys Ser	Leu Glu		
161		140		145		150
162	Cys Thr Lys Leu Cys	Leu Pro Gln Ile	Glu Asn			
163		155		160		
164						

165 (2) INFORMATION FOR SEQ ID NO:5:

166

167 (i) SEQUENCE CHARACTERISTICS:

--> 168 (A) LENGTH:157 bases

169 (B) TYPE:nucleic acid

170 (C) STRANDEDNESS:single

171 (D) TOPOLOGY:linear

172

173 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

174

175 CAGGGGAAA ATATTCACCC TCAAATAAT TCGATTTGCT GTACCAAGTG

176

50 CCACAAAGG AAACACTTG TA

177 (2) INFORMATION FOR SEQ ID NO:6:

178

179 (i) SEQUENCE CHARACTERISTICS:

--> 180 (A) LENGTH:13 amino acids

--> 181 (B) TYPE:polypeptide

182

--> 183 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

184

185 Asp Ser Val Xaa Pro Gln Gly Lys Tyr Ile His Pro Gln

186

187

188 (2) INFORMATION FOR SEQ ID NO:7:

189

190 (i) SEQUENCE CHARACTERISTICS:

--> 191 (A) LENGTH:11 amino acids

--> 192 (B) TYPE:polypeptide

*insert  
hand  
returns*

*add (D) TOPOLOGY: and sequence*

*same error*

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/484,312DATE: 03/22/1999  
TIME: 13:47:00

INPUT SET: S31121.raw

193  
--> 194 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:  
195  
196 Glu Asn Glu Cys Val Ser Cys Ser Asn Cys Lys  
197 5 10  
198

---

199 (2) INFORMATION FOR SEQ ID NO:8:  
200  
201 (i) SEQUENCE CHARACTERISTICS:  
--> 202 (A) LENGTH:12 amino acids  
--> 203 (B) TYPE:polypeptide  
204  
--> 205 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:  
206  
207 Glu Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys  
208 5 10  
209

---

210 (2) INFORMATION FOR SEQ ID NO:9:  
211  
212 (i) SEQUENCE CHARACTERISTICS:  
--> 213 (A) LENGTH:13 amino acids  
--> 214 (B) TYPE:polypeptide  
215  
--> 216 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:  
217  
218 Tyr Ile His Pro Gln Xaa Asn Ser Ile Xaa Xaa Xaa Lys  
219 5 10  
220 (2) ← use this number for all sequences  
221 (11) INFORMATION FOR SEQ ID NO:10:  
222  
223 (i) SEQUENCE CHARACTERISTICS:  
--> 224 (A) LENGTH:14 amino acids  
--> 225 (B) TYPE:polypeptide  
226  
--> 227 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:  
228  
229 Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn Asn Lys  
230 5 10  
231

---

--> 232 (2) INFORMATION FOR SEQ ID NO:11:  
233  
234 (i) SEQUENCE CHARACTERISTICS:  
--> 235 (A) LENGTH:15 amino acids  
--> 236 (B) TYPE:polypeptide  
237  
--> 238 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:  
239  
240 Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg  
241 5 10 15  
242

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/484,312DATE: 03/22/1999  
TIME: 13:47:01

INPUT SET: S31121.raw

292  
293 (i) SEQUENCE CHARACTERISTICS:  
--> 294 (A) LENGTH:18 amino acids  
--> 295 (B) TYPE:polypeptide  
296  
--> 297 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:  
298  
299 Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr  
300 5 10 15  
301 Xaa Xaa Arg  
302  
303

304 (2) INFORMATION FOR SEQ ID NO:17:  
305  
306 (i) SEQUENCE CHARACTERISTICS:  
--> 307 (A) LENGTH:14 amino acids  
--> 308 (B) TYPE:polypeptide  
309  
--> 310 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:  
311  
312 Gln Asn Thr Val Cys Thr Xaa His Ala Gly Phe Phe Leu Arg  
313 5 10  
314

315 (2) INFORMATION FOR SEQ ID NO:18:  
316  
317 (i) SEQUENCE CHARACTERISTICS:  
--> 318 (A) LENGTH:14 amino acids  
--> 319 (B) TYPE:polypeptide  
320  
--> 321 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:  
322  
323 Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu Asn  
324 5 10  
325

326 (2) INFORMATION FOR SEQ ID NO:19:  
327  
328 (i) SEQUENCE CHARACTERISTICS:  
--> 329 (A) LENGTH:13 amino acids  
--> 330 (B) TYPE:polypeptide  
331  
--> 332 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:  
333  
334 Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln  
335 5 10  
336

481 (2) INFORMATION FOR SEQ ID NO:32:  
482  
483 (i) SEQUENCE CHARACTERISTICS:  
--> 484 (A) LENGTH:14 amino acids

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/484,312DATE: 03/22/1999  
TIME: 13:47:00

INPUT SET: S31121.raw

---

243 (2) INFORMATION FOR SEQ ID NO:12:  
244  
245 (i) SEQUENCE CHARACTERISTICS:  
--> 246 (A) LENGTH:13 amino acids  
--> 247 (B) TYPE:polypeptide  
248  
--> 249 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:  
250  
251 Gly Thr Tyr Ley Tyr Asn Asp Cys Pro Gly Pro Gly Gln  
252 5 10  
253

---

254 (2) INFORMATION FOR SEQ ID NO:13:  
255  
256 (i) SEQUENCE CHARACTERISTICS:  
--> 257 (A) LENGTH:13 amino acids  
--> 258 (B) TYPE:polypeptide  
259  
--> 260 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:  
261  
262 Glu Met Gly Gln Val Glu Ile Ser Xaa Xaa Xaa Val Asp  
263 5 10  
264

---

265 (2) INFORMATION FOR SEQ ID NO:14:  
266  
267 (i) SEQUENCE CHARACTERISTICS:  
--> 268 (A) LENGTH:20 amino acids  
--> 269 (B) TYPE:polypeptide  
270  
--> 271 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:  
272  
273 Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg  
274 5 10 15  
275 Asp Thr Val Cys Gly  
276 20  
277

---

278 (2) INFORMATION FOR SEQ ID NO:15:  
279  
280 (i) SEQUENCE CHARACTERISTICS:  
--> 281 (A) LENGTH:19 amino acids  
--> 282 (B) TYPE:polypeptide  
283  
--> 284 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:  
285  
286 Tyr Ile His Pro Gln Xaa Asn Ser Ile Cys Cys Thr Lys Cys His  
287 5 10 15  
288 Lys Gly Xaa Tyr  
289  
290

---

291 (2) INFORMATION FOR SEQ ID NO:16:

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/484,312DATE: 03/22/1999  
TIME: 13:47:01

INPUT SET: S31121.raw

--> 485 (B) TYPE:polypeptide *same*  
486  
--> 487 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:  
488  
489 Glu Cys Gly Ser Gly Ser Phe Thr Ala Ser Glu Asn Asn Lys  
490 5 10  
491

---

492 (2) INFORMATION FOR SEQ ID NO:33:  
493  
494 (i) SEQUENCE CHARACTERISTICS:  
--> 495 (A) LENGTH:14 amino acids  
--> 496 (B) TYPE:polypeptide *same*  
497  
--> 498 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:  
499  
500 Glu Cys Gly Ser Gly Ser Phe Thr Ala Ser Cys Asn Asn Lys  
501 5 10  
502

---

647 (2) INFORMATION FOR SEQ ID NO:46:  
648  
649 (i) SEQUENCE CHARACTERISTICS:  
--> 650 (A) LENGTH:51 amino acids *same*  
--> 651 (B) TYPE:polypeptide  
652  
--> 653 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:  
654  
655 Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr  
656 5 10 15  
657 Lys Cys His Lys Gly Thr Tyr Ley Tyr Asn Asp Cys Pro Gly Pro  
658 20 25 30  
659 Gly Gln Asp Thr Asp Cys Arg Gly Cys Glu Ser Gly Ser Phe Thr  
660 35 40 45  
661 Ala Ser Glu Asn Asn Lys  
662 50  
663

---

664 (2) INFORMATION FOR SEQ ID NO:47:  
665  
666 (i) SEQUENCE CHARACTERISTICS:  
--> 667 (A) LENGTH:158 bases  
668 (B) TYPE:nucleic acid  
669 (C) STRANDEDNESS:single  
670 (D) TOPOLOGY:linear  
671  
672 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:  
673  
674 CAGGGGAAAT ATATTCACCC TCAAATAAT TCGATTTCGT GTACCAAGTC 50 GCACAAAGGA ACCTACTTGT A  
675

---

762 (2) INFORMATION FOR SEQ ID NO:55:  
763

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/484,312DATE: 03/22/1999  
TIME: 13:47:01

INPUT SET: S31121.raw

--> 764 (i) SEQUENCE CHARACTERISTICS:  
765 (A) LENGTH:63 bases  
766 (B) TYPE:nucleic acid  
767 (C) STRANDEDNESS:single  
768 (D) TOPOLOGY:linear  
769  
770 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:  
771  
772 AGCTCTAGAG ATTCGCGGCC GCTCGAGGTA CCGGATCCAT CGATGTCGAC 50 CTGCAGAAGC TTG  
773

---

774 (2) INFORMATION FOR SEQ ID NO:56:  
775  
776 (i) SEQUENCE CHARACTERISTICS:  
--> 777 (A) LENGTH:64 bases  
778 (B) TYPE:nucleic acid  
779 (C) STRANDEDNESS:single  
780 (D) TOPOLOGY:linear  
781  
782 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:  
783  
784 CTAGCAAGCT TCTGCAGGTC GACATCGATG GATCCGGTAC CTCGAGCGGC 50 CGCGAATTCT CTAG  
785

---

810 (2) INFORMATION FOR SEQ ID NO:59:  
811  
812 (i) SEQUENCE CHARACTERISTICS:  
--> 813 (A) LENGTH:81 bases  
814 (B) TYPE:nucleic acid  
815 (C) STRANDEDNESS:single  
816 (D) TOPOLOGY:linear  
817  
818 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:  
819  
820 CACAGTCGAC TTACATTTGC TTCTGACACA ACTGTGTTCA CTAGCAACCT 50 CAAACAGACA CCATGGGCCT C  
821

---

870 (2) INFORMATION FOR SEQ ID NO:64:  
871  
872 (i) SEQUENCE CHARACTERISTICS:  
--> 873 (A) LENGTH:30 bases 18 slow  
874 (B) TYPE:nucleic acid  
875 (C) STRANDEDNESS:single  
876 (D) TOPOLOGY:linear  
877  
878 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:  
879  
880 GTCCAATTAT GTCACACC 18  
881

---

882 (2) INFORMATION FOR SEQ ID NO:65:  
883  
884 (i) SEQUENCE CHARACTERISTICS:

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/484,312

DATE: 03/22/1999  
TIME: 13:47:02

INPUT SET: S31121.raw

```

--> 885 (A) LENGTH:1334 bases
886 (B) TYPE:nucleic acid
887 (C) STRANDEDNESS:single
888 (D) TOPOLOGY:linear
889
890 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:
891
892 GAATTCTCTG GACTGAGGCT CCAGTTCTGG CCTTTGGGGT TCAAGATCAC 50 TGGGACCAGG CCGTGAT
893
--> 894 TAGCTGTCTG GC 212
895
896 ATG GGC CTC TCC ACC GTG CCT GAC CTG CTG CTG CCA CTG GTG TTC 257
897 Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu
898 5 10 15
899
900 CTG GAG CTG TTG GTG GGA ATA TAC CCC TCA GGG GTT ATT GGA CTG 302
901 Leu Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu
902 20 25 30
903
904 GTC CCT CAC CTA GGG GAC AGG GAG AAG AGA GAT AGT GTG TGT CCC 347
905 Val Pro His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro
906 35 40 45
907
908 CAA GGA AAA TAT ATC CAC CCT CAA AAT AAT TCG ATT TGC TGT ACC 392
909 Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr
910 50 55 60
911
912 AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC TGT CCA GGC CCG 437
913 Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro
914 65 70 75
915
916 GGG CAG GAT ACG GAC TGC AGG GAG TGT GAG AGC GGC TCC TTC ACC 482
917 Gly Gln Asp The Asp Cys Arg Glu Cys Gly Ser Gly Ser Phe Thr
918 80 85 90
919
920 GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC AGC TGC TCC AAA TGC 527
921 Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys
922 95 100 105
923
924 CGA AAG GAA ATC GGT CAG GTG GAG ATC TCT TCT TGC ACA GTG GAC 572
925 Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp
926 110 115 120
927
928 CGG GAC ACC GTG TGT GGC TGC AGG AAG AAC CAG TAC CGG CAT TAT 617
929 Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr
930 125 130 135
931
932 TGG AGT GAA AAC CTTTTC CAG TGC TTC AAT TGC AGC CTC TGC CTC 662
933 Trp Ser Glu Asn Leuphe Gln Cys Phe Asn Cys Ser Leu Cys Leu
934 140 145 150
935
936 AAT GGG ACC GTG CAC CTC TCC TGC CAG GAG AAA CAG AAC ACC GTG 707
937 Asn Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val

```

*spaces appear in submitted file - if there is a gap in the sequence, separate sequences must be shown (see 1.822(b) of Sequence Rules)*

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/484,312

DATE: 03/22/1999  
TIME: 13:47:02

INPUT SET: S31121.raw

938		155		160		165	
939							
940	TGC ACC TGC CAT GCA GGT TTC TTT CTA AGA GAA AAC GAG TGT GTC					752	
941	Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val						
942		170		175		180	
943							
944	TCC TGT AGT AAC TGT AAG AAA AGC CTG GAG TGC AGG AAG TTG TGC					797	
945	Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys						
946		185		190		195	
947							
948	CTA CCC CAG ATT GAG AAT GTT AAG GGC ACT GAG GAC TCA GGC ACC					842	
949	Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser Gly Thr						
950		200		205		210	
951							
952	ACA GTG CTG TTG CCC CTG GTC ATT TTC TTT GGT CTT TGC CTT TTA					887	
953	Thr Val Leu Leu ProLeu Val Ile Phe Phe Gly Leu Cys Leu Leu						
954		215	gor?	220		225	
955							
956	TCC CTC CTC TTC ATT GGT TTA ATG TAT CGC TAC CAA CGG TGG AAG					932	
957	Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys						
958		230		235		240	
959							
960	TCC AAG CTC TAC TCC ATT GTT TGT GGG AAA TCG ACA CCT GAA AAA					977	
961	Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys						
962		245		250		255	
963							
964	GAG GGG GAG CTT GAA GGA ACT ACT ACT AAG CCC CTG GCC CCA AAC					1022	
965	Glu Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn						
966		260		265		270	
967							
968	CCA AGC TTC AGT CCC ACT CCA GGC TTC ACC CCC ACC CTG GGC TTC					1067	
969	Pro Ser Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe						
970		275		280		285	
971							
972	AGT CCC GTG CCC AGT TCC ACC TTC ACC TCC AGC TCC ACC TAT ACC					1112	
973	Ser Pro Val Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr						
974		290		295		300	
975							
976	CCC GGT GAC TGT CCC AAC TTT GCG GCT CCC CGC AGA GAG GTG GCA					1157	
977	Pro Gly Asp Cys Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala						
978		305		310		315	
979							
980	CCA CCC TAT CAG GGG GCT GAC CCC ATC CTT GCG ACA GCC CTC GCC					1202	
981	Pro Pro Tyr Gln Gly Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala						
982		320		325		330	
983							
984	TCC GAC CCC ATC CCC AAC CCC CTT CAG AAG TGG GAG GAC AGC GCC					1247	
985	Ser Asp Pro Ile Pro Asn Pro Leu Gln Lys Trp Glu Asp Ser Ala						
986		335		340		345	
987							
988	CAC AAG CCA CAG AGC CTA GAC ACT GAT GAC CCC GCG ACG CTG TAC					1292	
989	His Lys Pro Gln Ser Leu Asp Thr Asp Asp Pro Ala Thr Leu Tyr						
990		350		355		360	

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/484,312

DATE: 03/22/1999  
TIME: 13:47:02

INPUT SET: S31121.raw

```

991
992 GCC GTG GTG GAG AAC GTG CCC CCG TTG CGC TGG AAGGAATTC      1334
993 Ala Val Val Glu Asn Val Pro Pro Leu Arg Trp
994                      365                      370
995
996

```

---

```

997 (2) INFORMATION FOR SEQ ID NO:66:
998
999 (i) SEQUENCE CHARACTERISTICS:
--> 1000 (A) LENGTH:371 amino acids
--> 1001 (B) TYPE:polypeptide
1002
--> 1003 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:
1004
1005 Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu
1006                      5                      10                      15
1007 Leu Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu
1008                      20                      25                      30
1009 Val Pro His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro
1010                      35                      40                      45
1011 Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr
1012                      50                      55                      60
1013 Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro
1014                      65                      70                      75
1015 Gly Gln Asp The Asp Cys Arg Glu Cys Gly Ser Gly Ser Phe Thr
1016                      80                      85                      90
1017 Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys
1018                      95                      100                     105
1019 Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp
1020                      110                     115                     120
1021 Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr
1022                      125                     130                     135
1023 Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu
1024                      140                     145                     150
1025 Asn Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val
1026                      155                     160                     165
1027 Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val
1028                      170                     175                     180
1029 Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys
1030                      185                     190                     195
1031 Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser Gly Thr
1032                      200                     205                     210
1033 Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu Leu
1034                      215                     220                     225
1035 Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
1036                      230                     235                     240
1037 Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys
1038                      245                     250                     255
1039 Glu Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn
1040                      260                     265                     270
1041 Pro Ser Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe
1042                      275                     280                     285

```

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/484,312DATE: 03/22/1999  
TIME: 13:47:03

INPUT SET: S31121.raw

1043	Ser Pro Val Pro	Ser Ser Thr Phe Thr	Ser Ser Ser Thr Tyr Thr
1044		290	295 300
1045	Pro Gly Asp Cys	Pro Asn Phe Ala Ala	Pro Arg Arg Glu Val Ala
1046		305	310 315
1047	Pro Pro Tyr Gln	Gly Ala Asp Pro Ile	Leu Ala Thr Ala Leu Ala
1048		320	325 330
1049	Ser Asp Pro Ile	Pro Asn Pro Leu Gln	Lys Trp Glu Asp Ser Ala
1050		335	340 345
1051	His Lys Pro Gln	Ser Leu Asp Thr Asp	Asp Pro Ala Thr Leu Tyr
1052		350	355 360
1053	Ala Val Val Glu	Asn Val Pro Pro Leu	Arg Trp
1054		365	370
1055			

1056 (2) INFORMATION FOR SEQ ID NO:67:

1057

1058 (i) SEQUENCE CHARACTERISTICS:

--&gt; 1059 (A) LENGTH:6464 bases

1060 (B) TYPE:nucleic acid

1061 (C) STRANDEDNESS:single

1062 (D) TOPOLOGY:linear

1063

1064 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

1065

1066	TCGACATTGA	TTATTGACTA	GTTATTAATA	GTAATCAATT	ACGGGGTCAT	50	
1067	TAGTTCATAG	CCCATATATG	GAGTTCGCG	TTACATAACT	TACGGTAAAT	100	GGCCCCGCTC GCTGACCGCC C
1068	CTGGCATTAT	GCCCACTACA	TGACCTTATG	GGACTTTCCT	ACTIGGCAGT	350	ACATCTACGT ATTAGTCATC G
1069	AGAACCCACT	GCTTAACTGG	CTTATCGAAA	TTAATACGAC	TCACTATAGG	650	GAGACCCAAG CTTCTGCAGG T
1070	AGGTTTTACT	TGCTTTAAAA	AACCTCCAC	ACCTCCCCCT	GAACCTGAAA	1250	CATAAAATGA ATGCAATTGT T
1071	GTTAAAAGAT	GTATCCTGGA	CCTGCCAGAC	CTGGCCATTC	ACGTAAACAG	1550	AAGATTCCGC CTCAGTTCC G
1072	CCCACCACCT	GGCCCCGCCC	CGTTGAGGAC	AGAAGAAACC	CCGGGCAGCC	1850	GCAGCCAAGG CGGACGGGTA G
1073	GCGGCCACGC	CGGACTGGGC	GGGGCCGGCC	TGGTGGAGGC	GGAGTCTGAC	2150	CTCGTGGAGG CGGGGCCCTCT G
1074	TGGCTGGATT	GGGTTAGGGA	AACCGAGGCG	GTTTCGCTGAA	TCGGGTCGAG	2450	CAC TTGGCGG AGACGCGCGG G
1075	GAACGAGTTC	AAGTACTTCC	AAAGAATGAC	CACCACCTCC	TCAGTGGAAG	2750	GTAAACAGAA CCTGGTGATT A
1076	AGGCCATCTC	AGACTCTTTG	TGACAAGGAT	CATGCAGGAA	TTTGAAAGTG	3050	ACACGTTCTT CCCAGAAATT G
1077	GCAGAGCTAG	AACTCAGACT	TTAAAGAAAA	TTAGATCAAA	GTAGAGACTG	3650	AATTATTCTG CACATCAGAC T
1078	ATGCATCTCA	ATTAGTCAGC	AACCAGGTGT	GGAAAGTCCC	CAGGCTCCCC	4000	AGCAGGCAGA AGTATGCAAA G
1079	CTGTAGCGGC	GCATTAAGCG	CGGCGGGTGT	GGTGGTTACG	CGCAGCGTGA	4255	CCGCTACACT TGCCAGCGCC C
1080	GTCGCCCTTA	TTCCCTTTTT	TGCGGCATTT	TGCCTTCCTG	TTTTTGTCTA	4850	CCCAGAAACG CTGGTGAAAG T
1081	GAAAAGCATC	TTACGGATGG	CATGACAGTA	AGAGKATTAT	GCAGTGCTGC	5150	CATAACCATG AGTGATAACA C
1082	TGGATGGAGG	CGGATAAAGT	TGCAGGACCA	CTTCTGCGCT	CGGCCCTTCC	5450	GGCTGGCTGG TTTATTGCTG A
1083	AAAAGGATCT	AGGTGAAGAT	CCTTTTTGAT	AATCTCATGA	CCAAAATCCC	5750	TTAACGTGAG TTTTCGTTCC A
1084	GTAGCACCGC	CTACATACCT	CGCTCTGCTA	ATCCTGTTAC	CAGTGGCTGC	6100	TGCCAGTGGC GATAAGTCGT G
1085	GGAAACGCCT	GGTATCTTTA	TAGTCCTGTC	GGGTTTCGCC	ACCTCTGACT	6400	TGAGCGTCGA TTTTTGTGAT G
1086							

1087 (2) INFORMATION FOR SEQ ID NO:68:

1088

1089 (i) SEQUENCE CHARACTERISTICS:

--&gt; 1090 (A) LENGTH:2173 bases

1091 (B) TYPE:nucleic acid

1092 (C) STRANDEDNESS:single

1093 (D) TOPOLOGY:linear

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/484,312

DATE: 03/22/1999  
TIME: 13:47:03

INPUT SET: S31121.raw

1094  
1095 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:  
1096  
1097 GAATTCCTTT TCTCCGAGTT TTCTGAACTC TGGCTCATGA TCGGGCTTAC 50 TGGATACGAG AATCCTG  
1098  
--> 1099 ATG GGT CTC CCC ATC GTG CCT GGC CTG CTG CTG TCA CTG GTG CTC 289  
1100 Met Gly Leu Pro Ile Val Pro Gly Leu Leu Leu Ser Leu Val Leu  
1101 5 10 15  
1102  
1103 CTG GCT CTG CTG ATG GGG ATA CAC CCA TCA GGG GTC ACC GGA CTG 334  
1104 Leu Ala Leu Leu Met Gly Ile His Pro Ser Gly Val Thr Gly Leu  
1105 20 25 30  
1106  
1107 GTT CCT TCT CTT GGT GAC CGG GAG AAG AGG GAT AAT TTG TGT CCC 379  
1108 Val Pro Ser Leu Gly Asp Ara Glu Lys Arg Asp Asn Leu Cys Pro  
1109 35 40 45  
1110  
1111 CAG GGA AAG TAT GCC CAT CCA AAG AAT AAT TCC ATC TGC TGC ACC 424  
1112 Gln Gly Lys Tyr Ala His Pro Lys Asn Asn Ser Ile Cys Cys Thr  
1113 50 55 60  
1114  
1115 AAG TGC CAC AAA GGA ACC TAC TTG GTG AGT GAC TGT CCA AGC CCA 469  
1116 Lys Cys His Lys Gly Thr Tyr Leu Val Ser Asp Cys Pro Ser Pro  
1117 65 70 75  
1118  
1119 GGG CAG GAA ACA GTC TGC GAG CTC TCT CAT AAA GGC ACC TTT ACA 514  
1120 Gly Gln Glu Thr Val Cys Glu Leu Ser His Lys Gly Thr Phe Thr  
1121 80 85 90  
1122  
1123 GCT TCG CAG AAC CAC GTC AGA CAG TGT CTC AGT TGC AAG ACA TGT 559  
1124 Ala Ser Gln Asn His Val Arg Gln Cys Leu Ser Cys Lys Thr Cys  
1125 95 100 105  
1126  
1127 CGG AAA GAA ATG TTC CAG GTG GAG ATT TCT CCT TGC AAA GCT GAC 604  
1128 Arg Lys Glu Yet Phe Gln Val Glu Ile Ser Pro Cys Lys Ala Asp  
1129 110 115 120  
1130  
--> 1131 ATG GAC ACC GTG TGT GGC TGC AAG *unsubstituted nucleic acid derivative* CAA TTC CAG CGC TAC 649  
1132 Met Asp Thr Val Cys Gly Cys Lys Lys Asn Gln Phe Gln Arg Tyr  
1133 125 130 *use upper-case letters* 135  
1134  
1135 CTG AGT GAG ACG CAT TTC CAG TGT GTG GAC TGC AGC CCC TGC TTC 694  
1136 Leu Ser Glu Thr His Phe Gln Cys Val Asp Cys Ser Pro Cys Phe  
1137 140 145 150  
1138  
1139 AAT GGC ACC GTG ACA ATC CCC TGT AAG GAG AAA CAG AAC ACC GTG 739  
1140 Asn Gly Thr Val Thr Ile Pro Cys Lys Glu Lys Gln Asn Thr Val  
1141 155 160 165  
1142  
1143 TGT AAC TGC CAC GCA GGA TTC TTT CTA AGC GGA AAT GAG TGC ACC 784  
1144 Cys Asn Cys His Ala Gly Phe Phe Leu Ser Gly Asn Glu Cys Thr  
1145 170 175 180  
1146

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/484,312

DATE: 03/22/1999  
TIME: 13:47:04

INPUT SET: S31121.raw

--> 1147 CCT TGC AGC CAC TGC AAG AAA AAT CAG GAA TGT ATG AAG CTG TGC 829  
1148 Pro Cys Ser His Cys Lys Lys Asn Gln Glu Cys Met Lys Leu Cys  
1149 185 190 195  
1150  
1151 CTA CCT CCA GTT GCA AAT GTC ACA AAC CCC CAG GAC TCA GGT ACT 874  
1152 Leu Pro Pro Val Ala Asn Val Thr Asn Pro Gln Asp Ser Gly Thr  
1153 200 205 210  
1154 *Invited for use in the sequence-<sup>use</sup> N and define in (IX) FEATURE: section'*  
1155 GCC GTC CTG TTG CCT CTG GTT ATC TTC CTA GGT CTT TGC CTT TTA 919  
1156 Ala Val Leu Leu Pro Leu Val Ile Phe Leu Gly Leu Cys Leu Leu  
1157 215 220 225  
1158  
1159 TTC TTT ATC TGC ATC AGT CTA CTG TGC CGA TAT CCC CAG TGG AGG 964  
1160 Phe Phe Ile Cys Ile Ser Leu Leu Cys Arg Tyr Pro Gln Trp Arg  
1161 230 235 240  
1162  
1163 CCC AGG GTC TAC TCC ATC ATT TGT AGG GAT TCA GCT CCT GTC AAA 1009  
1164 Pro Arg Val Tyr Ser Ile Ile Cys Arg Asp Ser Ala Pro Val Lys  
1165 245 250 255  
1166  
1167 GAG GTG GAG GGT GAA GGA ATT GTT ACT AAG CCC CTA ACT CCA GCC 1054  
1168 Glu Val Glu Gly Glu Gly Ile Val Thr Lys Pro Leu Thr Pro Ala  
1169 260 265 270  
1170  
1171 TCT ATC CCA GCC TTC AGC CCC AAC CCC GGC TTC AAC CCC ACT CTG 1099  
1172 Ser Ile Pro Ala Phe Ser Pro Asn Pro Gly Phe Asn Pro Thr Leu  
1173 275 280 285  
1174  
1175 GGC TTC AGC ACC ACC CCA CGC TTC AGT CAT CCT GTC TCC AGT ACC 1144  
1176 Gly Phe Ser Thr Thr Pro Arg Phe Ser His Pro Val Ser Ser Thr  
1177 290 295 300  
1178  
1179 CCC ATC AGC CCC GTC TTC GGT CCT AGT AAC TGG CAC AAC TTC GTG 1189  
1180 Pro Ile Ser Pro Val Phe Gly Pro Ser Asn Trp His Asn Phe Val  
1181 305 310 315  
1182  
1183 CCA CCT GTA AGA GAG GTG GTC CCA ACC CAG GGT GCT GAC CCT CTC 1234  
1184 Pro Pro Val Arg Glu Val Val Pro Thr Gln Gly Ala Asp Pro Leu  
1185 320 325 330  
1186  
1187 CTC TAC GGA TCC CTC AAC CCT GTG CCA ATC CCC GCC CCT GTT CGG 1279  
1188 Leu Tyr Gly Ser Leu Asn Pro Val Pro Ile Pro Ala Pro Val Arg  
1189 335 340 345  
1190  
1191 AAA TGG GAA GAC GTC GTC GCG GCC CAG CCA CAA CGG CTT GAC ACT 1324  
1192 Lys Trp Glu Asp Val Val Ala Ala Gln Pro Gln Arg Leu Asp Thr  
1193 350 355 360  
1194  
1195 GCA GAC CCT GCG ATG CTG TAT GCT GTG GTG GAT GGC GTG CCT CCG 1369  
1196 Ala Asp Pro Ala Met Leu Tyr Ala Val Val Asp Gly Val Pro Pro  
1197 365 370 375  
1198  
1199 ACA CGC TGG AAG GAG TTC ATG CGG CTC CTG GGG CTG AGC GAG CAC 1414

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/484,312DATE: 03/22/1999  
TIME: 13:47:04

INPUT SET: S31121.raw

```
1200 Thr Arg Trp Lys Glu Phe Met Arg Leu Leu Gly Leu Ser Glu His
1201                               380                               385                               390
1202
1203 GAG ATC GAG CGG TTG GAG CTG CAG AAC GGG CGT TGC CTC CGC GAG 1459
1204 Glu Ile Glu Arc Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu
1205                               395                               400                               405
1206
1207 GCT CAT TAC AGC ATG CTG GAA GCC TGG CGG CGC CGC ACA CCG CGA 1504
1208 Ala His Tyr Ser Met Leu Glu Ala Trp Arg Arg Arg Thr Pro Arg
1209                               410                               415                               420
1210
1211 CAC GAG GCC ACG CTG GAC GTA GTG GGC CGC GTG CTT TGC GAC ATG 1549
1212 His Glu Ala Thr Leu Asp Val Val Gly Arg Val Leu Cys Asp Met
1213                               425                               430                               435
1214
1215 AAC CTG CGT GGC TGC CTG GAG AAC ATC CGC GAG ACT CTA GAA AGC 1594
1216 Asn Leu Arg Gly Cys Leu Glu Asn Ile Arg Glu Thr Leu Glu Ser
1217                               440                               445                               450
1218
1219 CCT GCC CAC TCG TCC ACG ACC CAC CTC CCG CGA TAAGGCCACA 1637
1220 Pro Ala His Ser Ser Thr Thr His Leu Pro Arg
1221                               455                               460
1222
1223 CCCCCACCTC AGGAACGGGA CTCGAAGGAC CATCCTGCTA GATGCCCTGC 1687
--> 1224 GGGAAAGTGTG CCATCTGCTC CCAGACAGCT GAGGGTGCCA AAAGCCAGGA 1887
1225 GAGGTGATTG TGGAGAAAAA GCACAATCTA TCTGATACCC ACTTGGGATG 1937
1226 CAAGGACCCA AACAAAGCTT CTCAGGGCCT CCTCAGTTGA TTTCTGGGCC 1987
1227 CTTTTCACAG TAGATAAAAC AGTCTTTGTA TTGATTATAT CACACTAATG 2037
1228 GATGAACGGT TGAAGTCCCT AAGGTAGGGG CAAGCACAGA ACAGTGGGGT 2087
1229 CTCCAGCTGG AGCCCCCGAC TCTTGTAAT ACATAAAAAA TCTAAAAGTG 2137
1230 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA GAATTC 2173
1231

1232 (2) INFORMATION FOR SEQ ID NO:69:
1233
1234 (i) SEQUENCE CHARACTERISTICS:
--> 1235 (A) LENGTH:461 amino acids
--> 1236 (B) TYPE:polypeptide
1237
--> 1238 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:
1239
1240 Met Gly Leu Pro Ile Val Pro Gly Leu Leu Leu Ser Leu Val Leu
1241                               5                               10                               15
1242 Leu Ala Leu Leu Met Gly Ile His Pro Ser Gly Val Thr Gly Leu
1243                               20                               25                               30
1244 Val Pro Ser Leu Gly Asp Ara Glu Lys Arg Asp Asn Leu Cys Pro
1245                               35                               40                               45
1246
1247 Gln Gly Lys Tyr Ala His Pro Lys Asn Asn Ser Ile Cys Cvs Thr
1248                               50                               55                               60
1249 Lys Cys His Lys Gly Thr Tyr Leu Val Ser Asp Cys Pro Ser Pro
1250                               65                               70                               75
1251 Gly Gln Glu Thr Val Cys Glu Leu Ser His Lys Gly Thr Phe Thr
```

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/484,312

DATE: 03/22/1999  
TIME: 13:47:04

INPUT SET: S31121.raw

1252		80		85		90
1253	Ala Ser Gln Asn His Val Arg Gln Cys Leu Ser Cys Lys Thr Cys					
1254		95		100		105
1255	Arg Lys Glu Yet Phe Gln Val Glu Ile Ser Pro Cys Lys Ala Asp					
1256		110		115		120
1257	Met Asp Thr Val Cys Gly Cys Lys Lys Asn Gln Phe Gln Arg Tyr					
1258		125		130		135
1259	Leu Ser Glu Thr His Phe Gln Cys Val Asp Cys Ser Pro Cys Phe					
1260		140		145		150
1261	Asn Gly Thr Val Thr Ile Pro Cys Lys Glu Lys Gln Asn Thr Val					
1262		155		160		165
1263	Cys Asn Cys His Ala Gly Phe Phe Leu Ser Gly Asn Glu Cys Thr					
1264		170		175		180
1265	Pro Cys Ser His Cys Lys Lys Asn Gln Glu Cys Met Lys Leu Cys					
1266		185		190		195
1267	Leu Pro Pro Val Ala Asn Val Thr Asn Pro Gln Asp Ser Gly Thr					
1268		200		205		210
1269	Ala Val Leu Leu Pro Leu Val Ile Phe Leu Gly Leu Cys Leu Leu					
1270		215		220		225
1271	Phe Phe Ile Cys Ile Ser Leu Leu Cys Arg Tyr Pro Gln Trp Arg					
1272		230		235		240
1273	Pro Arg Val Tyr Ser Ile Ile Cys Arg Asp Ser Ala Pro Val Lys					
1274		245		250		255
1275	Glu Val Glu Gly Glu Gly Ile Val Thr Lys Pro Leu Thr Pro Ala					
1276		260		265		270
1277	Ser Ile Pro Ala Phe Ser Pro Asn Pro Gly Phe Asn Pro Thr Leu					
1278		275		280		285
1279	Gly Phe Ser Thr Thr Pro Arg Phe Ser His Pro Val Ser Ser Thr					
1280		290		295		300
1281	Pro Ile Ser Pro Val Phe Gly Pro Ser Asn Trp His Asn Phe Val					
1282		305		310		315
1283	Pro Pro Val Arg Glu Val Val Pro Thr Gln Gly Ala Asp Pro Leu					
1284		320		325		330
1285	Leu Tyr Gly Ser Leu Asn Pro Val Pro Ile Pro Ala Pro Val Arg					
1286		335		340		345
1287	Lys Trp Glu Asp Val Val Ala Ala Gln Pro Gln Arg Leu Asp Thr					
1288		350		355		360
1289	Ala Asp Pro Ala Met Leu Tyr Ala Val Val Asp Gly Val Pro Pro					
1290		365		370		375
1291	Thr Arg Trp Lys Glu Phe Met Arg Leu Leu Gly Leu Ser Glu His					
1292		380		385		390
1293	Glu Ile Glu Arc Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu					
1294		395		400		405
1295	Ala His Tyr Ser Met Leu Glu Ala Trp Arg Arg Arg Thr Pro Arg					
1296		410		415		420
1297	His Glu Ala Thr Leu Asp Val Val Gly Arg Val Leu Cys Asp Met					
1298		425		430		435
1299	Asn Leu Arg Gly Cys Leu Glu Asn Ile Arg Glu Thr Leu Glu Ser					
1300		440		445		450
1301	Pro Ala His Ser Ser Thr Thr His Leu Pro Arg					
1302		455		460		
1303						

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/484,312

 DATE: 03/22/1999  
 TIME: 13:47:05

INPUT SET: S31121.raw

```

1413
1414 (i) SEQUENCE CHARACTERISTICS:
--> 1415 (A) LENGTH:340 amino acids
--> 1416 (B) TYPE:polypeptide
1417
--> 1418 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:
1419
1420 Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu
1421                               5              10              15
1422 Leu Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu
1423                               20              25              30
1424 Val Pro His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro
1425                               35              40              45
1426
1427 Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr
1428                               50              55              60
1429 Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro
1430                               65              70              75
1431 Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr
1432                               80              85              90
1433 Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys
1434                               95             100             105
1435 Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp
1436                               110            115            120
1437 Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr
1438                               125            130            135
1439 Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu
1440                               140            145            150
1441 Asn Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val
1442                               155            160            165
1443 Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val
1444                               170            175            180
1445 Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys
1446                               185            190            195
1447 Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser Gly Thr
1448                               200            205            210
1449 Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu Leu
1450                               215            220            225
1451 Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
1452                               230            235            240
1453 Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys
1454                               245            250            255
1455 Glu Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn
1456                               260            265            270
1457 Pro Ser Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe
1458                               275            280            285
1459 Ser Pro Val Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr
1460                               290            295            300
1461 Pro Gly Asp Cys Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala
1462                               305            310            315
1463 Pro Pro Tyr Gln Gly Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala
1464                               320            325            330
1465 Ser Asp Pro Ile Pro Asn Pro Leu Gln Lys
  
```

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/484,312DATE: 03/22/1999  
TIME: 13:47:05

INPUT SET: S31121.raw

1466  
1467  
1468

335

340

---

1469 (2) INFORMATION FOR SEQ ID NO:72:

1470

1471 (i) SEQUENCE CHARACTERISTICS:

1472 (A) LENGTH:19 bases

1473 (B) TYPE:nucleic acid

1474 (C) STRANDEDNESS:single

1475 (D) TOPOLOGY:linear

1476

1477 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

1478

1479 GTACTTGAAC TCGTTCCTG

19

1480

1481

1482

1483

1484

1485

1486

1487

---

*last sequence in file*

# SEQUENCE VERIFICATION REPORT

## PATENT APPLICATION US/08/484,312

DATE: 03/22/1999  
TIME: 13:47:05

INPUT SET: S31121.raw

Line	Error	Original Text
9	Number of Sequences (64) Doesn't Equal Actual Count (71)	(iii) NUMBER OF SEQUENCES:64
42	Entered (1365) and Calc. Seq. Length (0) differ	(A) LENGTH:1365 bases
54	Entered (483) and Calc. Seq. Length (0) differ	(A) LENGTH:483 bases
66	Entered (455) and Calc. Seq. Length (0) differ	(A) LENGTH:455 amino acids
67	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
69	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
69	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
137	Entered (161) and Calc. Seq. Length (0) differ	(A) LENGTH:161 amino acids
138	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
140	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
140	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
168	Entered (157) and Calc. Seq. Length (0) differ	(A) LENGTH:157 bases
180	Entered (13) and Calc. Seq. Length (0) differ	(A) LENGTH:13 amino acids
181	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
183	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
183	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
191	Entered (11) and Calc. Seq. Length (0) differ	(A) LENGTH:11 amino acids
192	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
194	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
194	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
202	Entered (12) and Calc. Seq. Length (0) differ	(A) LENGTH:12 amino acids
203	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
205	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
205	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
213	Entered (13) and Calc. Seq. Length (0) differ	(A) LENGTH:13 amino acids
214	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
216	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
216	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
224	Entered (14) and Calc. Seq. Length (0) differ	(A) LENGTH:14 amino acids
225	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
227	Wrong Sequence Number	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
227	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
227	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
232	Sequence * missing	(12) INFORMATION FOR SEQ ID NO:11:
235	Entered (15) and Calc. Seq. Length (0) differ	(A) LENGTH:15 amino acids
236	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
238	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
238	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
246	Entered (13) and Calc. Seq. Length (0) differ	(A) LENGTH:13 amino acids
247	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
249	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
249	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
257	Entered (13) and Calc. Seq. Length (0) differ	(A) LENGTH:13 amino acids
258	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
260	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
260	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
268	Entered (20) and Calc. Seq. Length (0) differ	(A) LENGTH:20 amino acids
269	Wrong or Missing Sequence Type	(B) TYPE:polypeptide

# SEQUENCE VERIFICATION REPORT

## PATENT APPLICATION US/08/484,312

DATE: 03/22/1999  
TIME: 13:47:06

INPUT SET: S31121.raw

Line	Error	Original Text
271	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
271	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
281	Entered (19) and Calc. Seq. Length (0) differ	(A) LENGTH:19 amino acids
282	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
284	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
284	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
294	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH:18 amino acids
295	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
297	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:
297	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:
307	Entered (14) and Calc. Seq. Length (0) differ	(A) LENGTH:14 amino acids
308	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
310	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:
310	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:
318	Entered (14) and Calc. Seq. Length (0) differ	(A) LENGTH:14 amino acids
319	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
321	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:
321	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:
329	Entered (13) and Calc. Seq. Length (0) differ	(A) LENGTH:13 amino acids
330	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
332	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:
332	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:
484	Entered (14) and Calc. Seq. Length (0) differ	(A) LENGTH:14 amino acids
485	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
487	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:
487	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:
495	Entered (14) and Calc. Seq. Length (0) differ	(A) LENGTH:14 amino acids
496	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
498	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:
498	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:
650	Entered (51) and Calc. Seq. Length (0) differ	(A) LENGTH:51 amino acids
651	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
653	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:
653	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:
667	Entered (158) and Calc. Seq. Length (0) differ	(A) LENGTH:158 bases
765	Entered (63) and Calc. Seq. Length (0) differ	(A) LENGTH:63 bases
777	Entered (64) and Calc. Seq. Length (0) differ	(A) LENGTH:64 bases
813	Entered (81) and Calc. Seq. Length (0) differ	(A) LENGTH:81 bases
873	Entered (30) and Calc. Seq. Length (18) differ	(A) LENGTH:30 bases
885	Entered (1334) and Calc. Seq. Length (1134) differ	(A) LENGTH:1334 bases
894	# of Sequences for line conflicts w/ running total	TAGCTGTCTG GC
1000	Entered (371) and Calc. Seq. Length (0) differ	(A) LENGTH:371 amino acids
1001	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
1003	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:
1003	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:
1059	Entered (6464) and Calc. Seq. Length (50) differ	(A) LENGTH:6464 bases
1090	Entered (2173) and Calc. Seq. Length (1727) differ	(A) LENGTH:2173 bases
1099	# of Sequences for line conflicts w/ running total	ATG GGT CTC CCC ATC GTG CCT GGC CTG CTG CT

**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/08/484,312**DATE: 03/22/1999  
TIME: 13:47:06**INPUT SET: S31121.raw**

Line	Error	Original Text
1131	Wrong Nucleic Acid Designator	ATG GAC ACC GTG TGT GGC TGC AAG PAG AkC CA
1131	# of Sequences for line conflicts w/ running total	ATG GAC ACC GTG TGT GGC TGC AAG PAG AkC CA
1155	Wrong Nucleic Acid Designator	GCC GIC CTG TTG CCT CTG GTT ATC TTC CTA GGT
1155	# of Sequences for line conflicts w/ running total	GCC GIC CTG TTG CCT CTG GTT ATC TTC CTA GGT
1224	# of Sequences for line conflicts w/ running total	GGGAAGTGTG CCATCTGCTC CCAGACAGCT GAGGG
1235	Entered (461) and Calc. Seq. Length (0) differ	(A) LENGTH:461 amino acids
1236	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
1238	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:
1238	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:
1415	Entered (340) and Calc. Seq. Length (0) differ	(A) LENGTH:340 amino acids
1416	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
1418	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:
1418	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71: